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Sequence Listing was accepted with existing errors.

See attached Validation Report.

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217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Tue Aug 14 11:56:41 EDT 2007

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Application No: 10587769

Version No: 1.1

Input Set:

Output Set:

Started: 2007-08-14 11:55:52.533

Finished: 2007-08-14 11:55:55.389

Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 856 ms

Total Warnings: 61

Total Errors: 1

No. of SeqIDs Defined: 80

Actual SeqID Count: 80

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)

**Input Set:**

**Output Set:**

**Started:** 2007-08-14 11:55:52.533  
**Finished:** 2007-08-14 11:55:55.389  
**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 856 ms  
**Total Warnings:** 61  
**Total Errors:** 1  
**No. of SeqIDs Defined:** 80  
**Actual SeqID Count:** 80

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

E 257

Invalid sequence data feature in <221> in SEQ ID (25)

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<110> Saribas, Sami  
Hakes, David  
Willet, Scott  
Johnson, Karl F.  
Bezila, Daniel James  
DeFrees, Shawn  
Neose Technologies, Inc.

<120> Methods of Refolding Mammalian Glycosyltransferases

<130> 019957-016830US

<140> US 10/587,769

<141> 2006-07-28

<150> US 60/542,210

<151> 2004-02-04

<150> US 60/599,406

<151> 2004-08-06

<150> US 60/627,406

<151> 2004-11-12

<150> WO PCT/US05/03856

<151> 2005-02-04

<160> 80

<170> PatentIn Ver. 2.1

<210> 1

<211> 445

<212> PRT

<213> Homo sapiens

<220>

<223> human beta-1,2-N-acetylglucosaminyltransferase I  
(GnTI, GnT1)

<400> 1

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1 5 10 15

Phe Val Ala Trp Asn Ala Leu Leu Leu Leu Phe Phe Trp Thr Arg Pro  
20 25 30

Ala Pro Gly Arg Pro Pro Ser Val Ser Ala Leu Asp Gly Asp Pro Ala  
35 40 45

Ser Leu Thr Arg Glu Val Ile Arg Leu Ala Gln Asp Ala Glu Val Glu  
50 55 60

Leu Glu Arg Gln Arg Gly Leu Leu Gln Gln Ile Gly Asp Ala Leu Ser  
65 70 75 80

Ser Gln Arg Gly Arg Val Pro Thr Ala Ala Pro Pro Ala Gln Pro Arg  
 85 90 95

Val Pro Val Thr Pro Ala Pro Ala Val Ile Pro Ile Leu Val Ile Ala  
 100 105 110

Cys Asp Arg Ser Thr Val Arg Arg Cys Leu Asp Lys Leu Leu His Tyr  
 115 120 125

Arg Pro Ser Ala Glu Leu Phe Pro Ile Ile Val Ser Gln Asp Cys Gly  
 130 135 140

His Glu Glu Thr Ala Gln Ala Ile Ala Ser Tyr Gly Ser Ala Val Thr  
 145 150 155 160

His Ile Arg Gln Pro Asp Leu Ser Ser Ile Ala Val Pro Pro Asp His  
 165 170 175

Arg Lys Phe Gln Gly Tyr Tyr Lys Ile Ala Arg His Tyr Arg Trp Ala  
 180 185 190

Leu Gly Gln Val Phe Arg Gln Phe Arg Phe Pro Ala Ala Val Val Val  
 195 200 205

Glu Asp Asp Leu Glu Val Ala Pro Asp Phe Phe Glu Tyr Phe Arg Ala  
 210 215 220

Thr Tyr Pro Leu Leu Lys Ala Asp Pro Ser Leu Trp Cys Val Ser Ala  
 225 230 235 240

Trp Asn Asp Asn Gly Lys Glu Gln Met Val Asp Ala Ser Arg Pro Glu  
 245 250 255

Leu Leu Tyr Arg Thr Asp Phe Phe Pro Gly Leu Gly Trp Leu Leu Leu  
 260 265 270

Ala Glu Leu Trp Ala Glu Leu Glu Pro Lys Trp Pro Lys Ala Phe Trp  
 275 280 285

Asp Asp Trp Met Arg Arg Pro Glu Gln Arg Gln Gly Arg Ala Cys Ile  
 290 295 300

Arg Pro Glu Ile Ser Arg Thr Met Thr Phe Gly Arg Lys Gly Val Ser  
 305 310 315 320

His Gly Gln Phe Phe Asp Gln His Leu Lys Phe Ile Lys Leu Asn Gln  
 325 330 335

Gln Phe Val His Phe Thr Gln Leu Asp Leu Ser Tyr Leu Gln Arg Glu  
 340 345 350

Ala Tyr Asp Arg Asp Phe Leu Ala Arg Val Tyr Gly Ala Pro Gln Leu  
 355 360 365

Gln Val Glu Lys Val Arg Thr Asn Asp Arg Lys Glu Leu Gly Glu Val  
 370 375 380

Arg Val Gln Tyr Thr Gly Arg Asp Ser Phe Lys Ala Phe Ala Lys Ala  
385 390 395 400

Leu Gly Val Met Asp Asp Leu Lys Ser Gly Val Pro Arg Ala Gly Tyr  
405 410 415

Arg Gly Ile Val Thr Phe Gln Phe Arg Gly Arg Arg Val His Leu Ala  
420 425 430

Pro Pro Pro Thr Trp Glu Gly Tyr Asp Pro Ser Trp Asn  
435 440 445

<210> 2

<211> 447

<212> PRT

<213> *Oryctolagus cuniculus*

<220>

<223> rabbit beta-1,2-N-acetylglucosaminyltransferase I  
(GnTI, GnT1)

<400> 2

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1 5 10 15

Phe Val Ala Trp Asn Ala Leu Leu Leu Leu Phe Phe Trp Thr Arg Pro  
20 25 30

Val Pro Ser Arg Leu Pro Ser Asp Asn Ala Leu Asp Asp Asp Pro Ala  
35 40 45

Ser Leu Thr Arg Glu Val Ile Arg Leu Ala Gln Asp Ala Glu Val Glu  
50 55 60

Leu Glu Arg Gln Arg Gly Leu Leu Gln Gln Ile Arg Glu His His Ala  
65 70 75 80

Leu Trp Ser Gln Arg Trp Lys Val Pro Thr Ala Ala Pro Pro Ala Gln  
85 90 95

Pro His Val Pro Val Thr Pro Pro Pro Ala Val Ile Pro Ile Leu Val  
100 105 110

Ile Ala Cys Asp Arg Ser Thr Val Arg Arg Cys Leu Asp Lys Leu Leu  
115 120 125

His Tyr Arg Pro Ser Ala Glu Leu Phe Pro Ile Ile Val Ser Gln Asp  
130 135 140

Cys Gly His Glu Glu Thr Ala Gln Val Ile Ala Ser Tyr Gly Ser Ala  
145 150 155 160

Val Thr His Ile Arg Gln Pro Asp Leu Ser Asn Ile Ala Val Gln Pro  
165 170 175

Asp	His	Arg	Lys	Phe	Gln	Gly	Tyr	Tyr	Lys	Ile	Ala	Arg	His	Tyr	Arg	180	185	190
Trp	Ala	Leu	Gly	Gln	Ile	Phe	His	Asn	Phe	Asn	Tyr	Pro	Ala	Ala	Val	195	200	205
Val	Val	Glu	Asp	Asp	Leu	Glu	Val	Ala	Pro	Asp	Phe	Phe	Glu	Tyr	Phe	210	215	220
Gln	Ala	Thr	Tyr	Pro	Leu	Leu	Lys	Ala	Asp	Pro	Ser	Leu	Trp	Cys	Val	225	230	235
Ser	Ala	Trp	Asn	Asp	Asn	Gly	Lys	Glu	Gln	Met	Val	Asp	Ser	Ser	Lys	245	250	255
Pro	Glu	Leu	Leu	Tyr	Arg	Thr	Asp	Phe	Phe	Pro	Gly	Leu	Gly	Trp	Leu	260	265	270
Leu	Leu	Ala	Glu	Leu	Trp	Ala	Glu	Leu	Glu	Pro	Lys	Trp	Pro	Lys	Ala	275	280	285
Phe	Trp	Asp	Asp	Trp	Met	Arg	Arg	Pro	Glu	Gln	Arg	Lys	Gly	Arg	Ala	290	295	300
Cys	Val	Arg	Pro	Glu	Ile	Ser	Arg	Thr	Met	Thr	Phe	Gly	Arg	Lys	Gly	305	310	315
Val	Ser	His	Gly	Gln	Phe	Phe	Asp	Gln	His	Leu	Lys	Phe	Ile	Lys	Leu	325	330	335
Asn	Gln	Gln	Phe	Val	Pro	Phe	Thr	Gln	Leu	Asp	Leu	Ser	Tyr	Leu	Gln	340	345	350
Gln	Glu	Ala	Tyr	Asp	Arg	Asp	Phe	Leu	Ala	Arg	Val	Tyr	Gly	Ala	Pro	355	360	365
Gln	Leu	Gln	Val	Glu	Lys	Val	Arg	Thr	Asn	Asp	Arg	Lys	Glu	Leu	Gly	370	375	380
Glu	Val	Arg	Val	Gln	Tyr	Thr	Gly	Arg	Asp	Ser	Phe	Lys	Ala	Phe	Ala	385	390	395
Lys	Ala	Leu	Gly	Val	Met	Asp	Asp	Leu	Lys	Ser	Gly	Val	Pro	Arg	Ala	405	410	415
Gly	Tyr	Arg	Gly	Ile	Val	Thr	Phe	Leu	Phe	Arg	Gly	Arg	Arg	Val	His	420	425	430
Leu	Ala	Pro	Pro	Gln	Thr	Trp	Asp	Gly	Tyr	Asp	Pro	Ser	Trp	Thr		435	440	445

<210> 3

<211> 342

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

beta-1,2-N-acetylglucosaminyltransferase I (GnTI,  
GnT1) Cys121Ser mutant

<400> 3

Ala	Val	Ile	Pro	Ile	Leu	Val	Ile	Ala	Cys	Asp	Arg	Ser	Thr	Val	Arg
1				5					10					15	
Arg	Ser	Leu	Asp	Lys	Leu	Leu	His	Tyr	Arg	Pro	Ser	Ala	Glu	Leu	Phe
			20					25					30		
Pro	Ile	Ile	Val	Ser	Gln	Asp	Cys	Gly	His	Glu	Glu	Thr	Ala	Gln	Ala
			35					40					45		
Ile	Ala	Ser	Tyr	Gly	Ser	Ala	Val	Thr	His	Ile	Arg	Gln	Pro	Asp	Leu
			50				55					60			
Ser	Ser	Ile	Ala	Val	Pro	Pro	Asp	His	Arg	Lys	Phe	Gln	Gly	Tyr	Tyr
65					70					75				80	
Lys	Ile	Ala	Arg	His	Tyr	Arg	Trp	Ala	Leu	Gly	Gln	Val	Phe	Arg	Gln
				85					90					95	
Phe	Arg	Phe	Pro	Ala	Ala	Val	Val	Val	Glu	Asp	Asp	Leu	Glu	Val	Ala
			100					105					110		
Pro	Asp	Phe	Phe	Glu	Tyr	Phe	Arg	Ala	Thr	Tyr	Pro	Leu	Leu	Lys	Ala
			115					120				125			
Asp	Pro	Ser	Leu	Trp	Cys	Val	Ser	Ala	Trp	Asn	Asp	Asn	Gly	Lys	Glu
			130				135					140			
Gln	Met	Val	Asp	Ala	Ser	Arg	Pro	Glu	Leu	Leu	Tyr	Arg	Thr	Asp	Phe
145					150					155				160	
Phe	Pro	Gly	Leu	Gly	Trp	Leu	Leu	Leu	Ala	Glu	Leu	Trp	Ala	Glu	Leu
				165					170					175	
Glu	Pro	Lys	Trp	Pro	Lys	Ala	Phe	Trp	Asp	Asp	Trp	Met	Arg	Arg	Pro
			180					185					190		
Glu	Gln	Arg	Gln	Gly	Arg	Ala	Cys	Ile	Arg	Pro	Glu	Ile	Ser	Arg	Thr
			195				200					205			
Met	Thr	Phe	Gly	Arg	Lys	Gly	Val	Ser	His	Gly	Gln	Phe	Phe	Asp	Gln
			210				215					220			
His	Leu	Lys	Phe	Ile	Lys	Leu	Asn	Gln	Gln	Phe	Val	His	Phe	Thr	Gln
225					230					235				240	
Leu	Asp	Leu	Ser	Tyr	Leu	Gln	Arg	Glu	Ala	Tyr	Asp	Arg	Asp	Phe	Leu
				245					250					255	
Ala	Arg	Val	Tyr	Gly	Ala	Pro	Gln	Leu	Gln	Val	Glu	Lys	Val	Arg	Thr
				260				265						270	



Asn Asp Arg Lys Glu Leu Gly Glu Val Arg Val Gln Tyr Thr Gly Arg  
275 280 285

Asp Ser Phe Lys Ala Phe Ala Lys Ala Leu Gly Val Met Asp Asp Leu  
290 295 300

Lys Ser Gly Val Pro Arg Ala Gly Tyr Arg Gly Ile Val Thr Phe Gln  
305 310 315 320

Phe Pro Gly Arg Arg Val His Leu Ala Pro Pro Thr Trp Glu Gly  
325 330 335

Tyr Asp Pro Ser Trp Asn  
340

<210> 4

<211> 1029

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

beta-1,2-N-acetylglucosaminyltransferase I (GnTI,  
GnT1) Cys121Ser mutant

<400> 4

gcggtgattc ccatacctggt catcgccctgt gaccgcagca ctgttcggcg ctctctagac 60  
aagctgctgc attatcggcc ctcggtgag ctcttcccca tcatcgttag ccaggactgc 120  
gggcacgagg agacggccca ggccatcgcc tcctacggca gcgcggtcac gcacatccgg 180  
cagcccgacc tgagcagcat tgcggtgccg ccggaccacc gcaagttcca gggctactac 240  
aagatcgcgc gccactaccg ctgggcgctg ggccaggtct tccggcagtt tcgcttcccc 300  
gcgggcgtgg tgggtggagga tgacctggag gtggccccgg acttcttcga gtactttcgg 360  
gccacctatc cgtgctgaa ggccgacccc tccctgtggt gcgtctcggc ctggaatgac 420  
aacggcaagg agcagatggt ggacgccagc aggcctgagc tgctctaccg caccgacttt 480  
ttccctggcc tgggctggct gctgttgccc gagctctggg ctgagctgga gcccaagtgg 540  
ccaaaggcct tctgggacga ctggatgcgg cggccggagc agcggcaggg gcgggcctgc 600  
atacgccctg agatctcaag aacgatgacc ttggccgca aggggtgtgag ccacgggcag 660  
ttctttgacc agcacctcaa gtttatcaag ctgaaccagc agtttgtgca cttcaccag 720  
ctggacctgt cttacctgca gcgggaggcc tatgaccgag atttcctcgc ccgcgtctac 780  
ggtgctcccc agctgcaggt ggagaaagtg aggaccaatg accggaagga gctgggggag 840  
gtgcggtgac agtatacggg cagggacagc ttcaaggctt tcgccaaggc tctgggtgac 900  
atggatgacc ttaagtcggg ggttccgaga gctggctacc ggggtattgt caccttccag 960  
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tggaattag 1029

<210> 5

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:unpaired  
cysteine mutation Cys121Ser mutant region

<400> 5

Ser Thr Val Arg Arg Ser Leu Asp Lys Leu Leu His  
1 5 10

<210> 6

<211> 342

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

beta-1,2-N-acetylglucosaminyltransferase I (GnTI,  
GnT1) Cys121Asp mutant

<400> 6

Ala Val Ile Pro Ile Leu Val Ile Ala Cys Asp Arg Ser Thr Val Arg  
1 5 10 15

Arg Asp Leu Asp Lys Leu Leu His Tyr Arg Pro Ser Ala Glu Leu Phe  
20 25 30

Pro Ile Ile Val Ser Gln Asp Cys Gly His Glu Glu Thr Ala Gln Ala  
35 40 45

Ile Ala Ser Tyr Gly Ser Ala Val Thr His Ile Arg Gln Pro Asp Leu  
50 55 60

Ser Ser Ile Ala Val Pro Pro Asp His Arg Lys Phe Gln Gly Tyr Tyr  
65 70 75 80

Lys Ile Ala Arg His Tyr Arg Trp Ala Leu Gly Gln Val Phe Arg Gln  
85 90 95

Phe Arg Phe Pro Ala Ala Val Val Val Glu Asp Asp Leu Glu Val Ala  
100 105 110

Pro Asp Phe Phe Glu Tyr Phe Arg Ala Thr Tyr Pro Leu Leu Lys Ala  
115 120 125

Asp Pro Ser Leu Trp Cys Val Ser Ala Trp Asn Asp Asn Gly Lys Glu  
130 135 140

Gln Met Val Asp Ala Ser Arg Pro Glu Leu Leu Tyr Arg Thr Asp Phe  
145 150 155 160

Phe Pro Gly Leu Gly Trp Leu Leu Leu Ala Glu Leu Trp Ala Glu Leu  
165 170 175

Glu Pro Lys Trp Pro Lys Ala Phe Trp Asp Asp Trp Met Arg Arg Pro  
180 185 190

Glu Gln Arg Gln Gly Arg Ala Cys Ile Arg Pro Glu Ile Ser Arg Thr  
195 200 205

Met Thr Phe Gly Arg Lys Gly Val Ser His Gly Gln Phe Phe Asp Gln  
210 215 220

His Leu Lys Phe Ile Lys Leu Asn Gln Gln Phe Val His Phe Thr Gln  
225 230 235 240

Leu Asp Leu Ser Tyr Leu Gln Arg Glu Ala Tyr Asp Arg Asp Phe Leu  
245 250 255

Ala Arg Val Tyr Gly Ala Pro Gln Leu Gln Val Glu Lys Val Arg Thr  
260 265 270

Asn Asp Arg Lys Glu Leu Gly Glu Val Arg Val Gln Tyr Thr Gly Arg  
275 280 285

Asp Ser Phe Lys Ala Phe Ala Lys Ala Leu Gly Val Met Asp Asp Leu  
290 295 300

Lys Ser Gly Val Pro Arg Ala Gly Tyr Arg Gly Ile Val Thr Phe Gln  
305 310 315 320

Phe Pro Gly Arg Arg Val His Leu Ala Pro Pro Pro Thr Trp Glu Gly  
325 330 335

Tyr Asp Pro Ser Trp Asn  
340

<210> 7

<211> 1029

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

beta-1,2-N-acetylglucosaminyltransferase I (GnTI,  
GnT1) Cys121Asp mutant

<400> 7

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aagctgctgc attatcggcc ctcggtgag ctcttcccca tcatcgttag ccaggactgc 120  
gggcacgagg agacggccca ggccatcgcc tcctacggca gcgcggtcac gcacatccgg 180  
cagcccgacc tgagcagcat tgcggtgccg ccggaccacc gcaagttcca gggctactac 240  
aagatcgcg cccactaccg ctgggcgctg ggccaggtct tccggcagtt tcgcttcccc 300  
gcggccgtgg tgggtggagga tgacctggag gtggccccgg acttcttcga gtactttcgg 360  
gccacctatc cgctgctgaa ggccgacccc tcctgtggt gcgtctcggc ctggaatgac 420  
aacggcaagg agcagatggt ggacgccagc aggcctgagc tgctctaccg caccgacttt 480  
ttccctggcc tgggctggct gctgttgccc gagctctggg ctgagctgga gcccaagtgg 540  
ccaaaggcct tctgggacga ctggatgcgg cggccggagc agcggcaggg gcgggcctgc 600  
atacgccctg agatctcaag aacgatgacc tttggccgca aggggtgtgag ccacgggcag 660  
ttctttgacc agcacctcaa gtttatcaag ctgaaccagc agtttgtgca cttcacccag 720  
ctggacctgt cttacctgca gcgggaggcc tatgaccgag atttcctcgc ccgcgtctac 780  
ggtgctcccc agctgcaggt ggagaaagtg aggaccaatg accggaagga gctgggggag 840  
gtgcggtgac agtatacggg caggggacagc ttcaaggctt tcgccaaggc tctgggtgtc 900  
atggatgacc ttaagtccgg ggttccgaga gctggctacc ggggtattgt caccttcag 960  
ttcccgggcc gccgtgtcca cctggcgccc ccaccgacgt gggagggcta tgatcctagc 1020  
tggaattag